



SEQUENCE LISTING

<110> Anderson et al.

<120> CRYSTAL STRUCTURE OF GLUTAMATE RACEMASE (MURI)

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<140> US 10/729,571

<141> 2003-12-05

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His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
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Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Ser Ile Leu
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Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly	
20 25 30	
gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag	144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys	
35 40 45	
caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa	192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys	
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tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag	240

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gtg Val	cta Leu	ggg Gly 115	aca Thr	aaa Lys	gcg Ala	acg Thr	att Ile 120	caa Gln	tct Ser	aac Asn	gct Ala	tat Tyr 125	gac Asp	aac Asn	gcc Ala	384
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ttt Phe 145	gtg Val	cct Pro	ttg Leu	att Ile	gaa Glu 150	gaa Glu	agt Ser	att Ile	tta Leu	gag Glu 155	ggc Gly	gaa Glu	ttg Leu	tta Leu	gag Glu 160	480
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ggc Gly	tat Tyr	ttt Phe 195	atg Met	gag Glu	cat His	ttt Phe	gcc Ala 200	ctt Leu	cca Pro	acc Thr	ccc Pro	ccc Pro 205	cta Leu	ctc Leu	atc Ile	624
cat His	tcg Ser 210	ggc Gly	gat Asp	gct Ala	att Ile	gta Val 215	gaa Glu	tat Tyr	ttg Leu	cag Gln	caa Gln 220	aaa Lys	tac Tyr	acc Thr	ctt Leu	672
aag Lys 225	aaa Lys	aat Asn	gca Ala	cac His	gca Ala 230	ttc Phe	cct Pro	aaa Lys	gtg Val	gaa Glu 235	ttt Phe	cat His	gcg Ala	agt Ser	ggc Gly 240	720
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Asp	Ser	Ala 35	Arg	Val	Pro	Tyr	Gly 40	Thr	Lys	Asp	Pro	Thr 45	Thr	Ile	Lys	

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
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Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
165 170 175

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Thr Leu
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atc att tta ggt tgc Ile Ile Leu Gly Cys 180	acg cat ttt ccc Thr His Phe Pro 185	ttg atc gct caa Leu Ile Ala Gln 190	aaa att gag Lys Ile Glu	576
ggc tat ttt atg gag Gly Tyr Phe Met Glu 195	cat ttt gcc ctt His Phe Ala Leu 200	tta acg ccc ccc Leu Thr Pro Pro 205	cta ctc atc Leu Leu Ile	624
cat tct ggc gat gct His Ser Gly Asp Ala 210	att gta gaa tat Ile Val Glu Tyr 215	ttg caa caa aaa Leu Gln Gln Lys 220	tac gcc ctt Tyr Ala Leu	672
aag aaa aat gca cac Lys Lys Asn Ala His 225	tca ttc cct aaa Ser Phe Pro Lys 230	gtg gaa ttt cat Val Glu Phe His 235	gcg agc ggc Ala Ser Gly 240	720
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<213> H. pylori

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35 40 45
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly
50 55 60
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
65 70 75 80
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
85 90 95
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
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Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
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Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
130 135 140
Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
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Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
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Gly Tyr Phe Met Glu His Phe Ala Leu Leu Thr Pro Pro Leu Leu Ile
195 200 205
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
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Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
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caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gaa 192
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85 90 95
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Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
145 150 155 160
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Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Lys Val
165 170 175
atc att tta ggt tgc acg cat ttt ccc ttg atc gct cac caa att aag 576
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Lys
180 185 190
ggc tat ttt atg ggg cat ttt gcc ctt tca acg ccc ccc cta ctc atc 624
Gly Tyr Phe Met Gly His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
195 200 205

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		20						25					30		

Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys
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Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Glu
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	130					135					140				

Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu
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Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Lys	Ile	Leu	Pro	Lys	Val
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Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Lys
180 185 190

Gly Tyr Phe Met Gly His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
195 200 205

His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu
210 215 220

Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
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20 25 30

gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
35 40 45

caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa 192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
50 55 60

tta ttg att gtg gca tgc aac aca gcg agt gct ctg gct tta gaa gag 240
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atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc 288
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
85 90 95

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Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
100 105 110

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Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
115 120 125

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130 135 140

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act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val 165 170 175	528
atc att tta ggt tgt acg cat ttt ccc ttg atc gct caa aaa att gag Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu 180 185 190	576
ggc tat ttt atg gaa cat ttt gcc ttt cca acg ccc ccc cta ctc atc Gly Tyr Phe Met Glu His Phe Ala Phe Pro Thr Pro Pro Leu Leu Ile 195 200 205	624
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aag aaa aat gca cac gca tta cct aaa gtg gaa ttt cat gcg agc ggc Lys Lys Asn Ala His Ala Leu Pro Lys Val Glu Phe His Ala Ser Gly 225 230 235 240	720
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Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu 65 70 75 80
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Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu 100 105 110
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Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala

Page 20

115					120					125					
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Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Lys	Ile	Leu	Pro	Glu	Val
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Lys	Lys	Asn	Ala	His	Ala	Leu	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly
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Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly	
20 25 30	
gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag	144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys	
35 40 45	
caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa	192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys	
50 55 60	
tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag	240
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu	
65 70 75 80	
atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc	288

Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser		
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		115					120					125					
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Lys	Lys	Asn	Ala	His	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly		
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		20						25					30		

Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys
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Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Lys
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Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
130 135 140

Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
165 170 175

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
180 185 190

Gly Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Ile Leu Ile
195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
210 215 220

Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
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48

aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc
Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly

96

20					25					30						
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Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
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caa	ttt	ggc	tta	gag	gct	ttg	gat	ttt	ttc	aaa	ccg	cac	cag	att	aaa	192
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Lys	
	50					55					60					
tta	ttg	att	gta	gca	tgc	aac	aca	gcg	agc	gct	cta	gct	tta	gaa	gag	240
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
65					70					75				80		
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Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser	
				85					90					95		
att	tta	gcg	atc	aaa	caa	caa	gta	aaa	gat	aaa	aac	gcc	cct	att	tta	336
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu	
			100					105					110			
gtg	cta	ggg	aca	aaa	gcg	acg	att	caa	tct	aac	gct	tat	gac	aac	gcc	384
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala	
		115					120					125				
ctg	aaa	caa	caa	ggc	tat	ttg	aat	gtt	tcg	cat	tta	gcc	act	tct	ctt	432
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu	
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ttt	gtg	cct	ttg	att	gaa	gaa	agt	att	tta	gag	ggc	gaa	ttg	tta	gaa	480
Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu	
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Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Lys	Ile	Leu	Pro	Glu	Val	
				165					170					175		
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Ile	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu	
			180					185					190			
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Ser	Tyr	Phe	Met	Gly	His	Phe	Ala	Leu	Pro	Thr	Pro	Pro	Leu	Leu	Ile	
		195					200					205				
cat	tct	ggc	gat	gct	att	gtg	gaa	tat	ttg	cag	caa	aaa	tac	gcc	ctt	672
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu	
	210					215					220					
aag	aaa	aac	gca	cac	gca	ttc	cct	aaa	gtg	gaa	ttt	cat	gcg	agc	ggc	720
Lys	Lys	Asn	Ala	His	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly	
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gat	gtg	atc	tgg	cta	gaa	aaa	caa	gct	aaa	gaa	tgg	ctc	aaa	ttg	taa	768
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35 40 45
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
50 55 60
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
65 70 75 80
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
85 90 95
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
100 105 110
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
115 120 125
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
130 135 140
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
145 150 155 160
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
165 170 175
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
180 185 190
Ser Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
195 200 205
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
210 215 220
Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
225 230 235 240
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aaa agc ctt tta aaa gcg caa cta ttt gat gaa atc atc tat tat ggc	96
Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly	
20 25 30	
gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag	144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys	
35 40 45	
caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga	192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly	
50 55 60	
tta ttg att gtg gca tgc aac aca gcg agc gct ctg gct tta gaa gag	240
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu	
65 70 75 80	
atg caa aaa tat tcc aaa atc cct att gtg ggc gtg att gag cca agc	288
Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser	
85 90 95	
att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc ccc att tta	336
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu	
100 105 110	
gtg cta ggg aca aaa gcg acg atc caa tct aac gct tat gat aac gcc	384
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala	
115 120 125	
ctg aaa caa caa ggc tat ttg aac att tcg cat tta gcc act tct ctt	432
Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu	
130 135 140	
ttt gtg ccc ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa	480
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu	
145 150 155 160	
act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg	528
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val	
165 170 175	
atc att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag	576
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu	
180 185 190	
agc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc tta ctc atc	624
Ser Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile	
195 200 205	
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His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu	

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	35	40	45
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly			
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Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu			
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	100	105	110
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala			
	115	120	125
Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu			
	130	135	140
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu			
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Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val			
	165	170	175
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu			
	180	185	190

Ser Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
210 215 220

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Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
20 25 30

gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
35 40 45

caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac aaa att gaa 192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu
50 55 60

tta tta att gtg gca tgc aac aca gcg agc gct ctg gct tta gaa gag 240
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
65 70 75 80

atg caa aag cat tcc aaa atc ccc att gtg ggc gtg att gag cca agc 288
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
85 90 95

att tta gcg atc aaa caa caa gtg aaa gat aaa aac acc cct att tta 336
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Thr Pro Ile Leu
100 105 110

gtg cta ggg aca aaa gcg acg atc caa tct aac gct tac gat aac gcc 384
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
115 120 125

ctg aaa caa caa ggc tat ttg aag gtt tcg cat ttg gcc act tct ctt 432
Leu Lys Gln Gln Gly Tyr Lys Val Ser His Leu Ala Thr Ser Leu
130 135 140

ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa 480
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
145 150 155 160

act tgc atg cgt tat tat ttc act cca tta gaa atc tta cct gaa gtg	528
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val	
165 170 175	

gtt att tta ggc tgc acg cat ttt ccc ttg atc gct caa aaa att gag	576
Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu	
180 185 190	

ggc tat ttt atg gaa cat ttt gcc ctt cca acg ccc ccc cta ctc atc	624
Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile	
195 200 205	

cat tct ggc gac gct att gtg gga tat ttg cag caa aaa tac gcc ctt	672
His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu	
210 215 220	

aag aaa aac gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc	720
Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly	
225 230 235 240	

gat gta att tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa	768
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35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu
50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Thr Pro Ile Leu
100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
115 120 125

Leu Lys Gln Gln Gly Tyr Leu Lys Val Ser His Leu Ala Thr Ser Leu
130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
165 170 175

Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
195 200 205

His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu
210 215 220

Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
225 230 235 240

Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
245 250 255

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Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly	
20 25 30	
gat agc gct agg gtg cct tat ggc act aaa gac ccc acc acg atc aag	144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys	
35 40 45	
caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac aag att gaa	192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu	
50 55 60	
tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gaa	240
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu	
65 70 75 80	
atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gaa cca agc	288
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser	
85 90 95	

att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta	336
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu	
100 105 110	
gtg cta ggg aca aaa gcg acg att caa tct aac gct tat gac aac gcc	384
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala	
115 120 125	
ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt	432
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu	
130 135 140	
ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg cta gaa	480
Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu	
145 150 155 160	
act tgc atg cgt tat tat ttc act cca tta gag atc ttg cct gaa gtg	528
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val	
165 170 175	
gtt att tta ggc tgc acg cat ttt ccc ttg atc gct cac caa att gag	576
Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu	
180 185 190	
ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc	624
Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile	
195 200 205	
cat tct ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt	672
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu	
210 215 220	
aag aaa aac gca tgt gca ttc cct aaa gta gaa ttt cat gcg agc ggc	720
Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly	
225 230 235 240	
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35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu
50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
Page 31

65	70	75	80
Met Gln Lys His	Ser Lys Ile Pro Ile	Val Gly Val Ile	Glu Pro Ser
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	100	105	110
Val Leu Gly Thr	Lys Ala Thr Ile	Gln Ser Asn Ala	Tyr Asp Asn Ala
	115	120	125
Leu Lys Gln Gln	Gly Tyr Leu Asn Val	Ser His Leu Ala	Thr Ser Leu
	130	135	140
Phe Val Pro Leu	Ile Glu Glu Asn Ile	Leu Glu Gly Glu	Leu Leu Glu
	145	150	155
Thr Cys Met Arg	Tyr Tyr Phe Thr	Pro Leu Glu Ile	Leu Pro Glu Val
	165	170	175
Val Ile Leu Gly	Cys Thr His Phe	Pro Leu Ile Ala	His Gln Ile Glu
	180	185	190
Gly Tyr Phe Met	Glu His Phe Ala	Leu Ser Thr Pro	Pro Leu Leu Ile
	195	200	205
His Ser Gly Asp	Ala Ile Val Glu Tyr	Leu Gln Gln Lys	Tyr Ala Leu
	210	215	220
Lys Lys Asn Ala	Cys Ala Phe Pro	Lys Val Glu Phe	His Ala Ser Gly
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<221> CDS
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Lys Ser Leu Leu Lys Val Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly	
20 25 30	
gat agt gct agg gtg cct tat ggc act aaa gac ccc acc acg atc aag	144

Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
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Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Lys	Ile	Glu	
	50					55					60					
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Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Gly	Glu	
65					70					75				80		
atg	caa	aag	tat	tcc	aaa	atc	cct	att	gtg	ggc	gtg	att	gag	cca	agc	288
Met	Gln	Lys	Tyr	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser	
				85					90					95		
att	tta	gcg	atc	aaa	caa	caa	gta	aaa	gat	aaa	aac	gcc	cct	att	tta	336
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu	
			100					105					110			
gta	cta	ggg	aca	aaa	gcg	acg	att	cga	tcc	aac	gct	tat	gac	aac	gcc	384
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Arg	Ser	Asn	Ala	Tyr	Asp	Asn	Ala	
		115					120					125				
ctg	aaa	caa	caa	ggc	tat	ttg	aat	att	tcg	cat	tta	gcc	act	tct	ctt	432
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Ile	Ser	His	Leu	Ala	Thr	Ser	Leu	
	130					135					140					
ttt	gtg	cct	ttg	att	gaa	gaa	aat	att	tta	gag	ggc	gaa	ttg	cta	gaa	480
Phe	Val	Pro	Leu	Ile	Glu	Glu	Asn	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu	
145					150					155					160	
act	tgc	atg	cgt	tat	tat	ttc	act	cca	tta	gag	att	tta	cct	gaa	gtg	528
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val	
				165					170					175		
gtt	att	tta	ggt	tgc	acg	cat	ttt	ccc	ttg	atc	gct	cac	caa	att	gag	576
Val	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	His	Gln	Ile	Glu	
			180					185					190			
ggc	tat	ttt	atg	gag	cat	ttt	gcc	ctt	tca	acg	ccc	ccc	cta	ctc	atc	624
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Ser	Thr	Pro	Pro	Leu	Leu	Ile	
		195					200					205				
cat	tct	ggc	gat	gct	att	gtg	gaa	tat	ttg	caa	caa	aaa	tac	gcc	ctt	672
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu	
	210					215					220					
aag	aaa	aac	gca	tgc	gca	ttc	cct	aaa	gta	gaa	ttc	cat	gcg	agc	ggc	720
Lys	Lys	Asn	Ala	Cys	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly	
225					230					235					240	
gat	gta	att	tggt	cta	gaa	aaa	cag	gct	aaa	gaa	tggt	ctc	aaa	ttg	taa	768
Asp	Val	Ile	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu		
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 <212> PRT
 <213> H. pylori

<400> 30

Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu
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 20 25 30
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu
 50 55 60
 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Gly Glu
 65 70 75 80
 Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 85 90 95
 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
 100 105 110
 Val Leu Gly Thr Lys Ala Thr Ile Arg Ser Asn Ala Tyr Asp Asn Ala
 115 120 125
 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
 130 135 140
 Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160
 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
 165 170 175
 Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu
 180 185 190
 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
 195 200 205
 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
 210 215 220
 Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240
 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
 245 250 255

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<213> H. pylori

<221> CDS

<222> (1)..(768)

<400> 31

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Met	Lys	Ile	Gly	Val	Phe	Asp	Ser	Gly	Val	Gly	Gly	Phe	Ser	Val	Leu	
1			5						10					15		

aaa	agc	ctt	tta	aaa	gcg	caa	att	ttt	gat	gaa	atc	atc	tat	tat	ggc	96
Lys	Ser	Leu	Leu	Lys	Ala	Gln	Ile	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
			20					25					30			

gat	agt	gct	aga	gtg	cct	tat	ggc	act	aaa	gac	ccc	acc	acg	atc	aag	144
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys	
		35					40					45				

caa	ttt	ggc	tta	gag	gct	ttg	gat	ttt	ttc	aaa	ccg	cac	cag	att	gga	192
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Gln	Ile	Gly	
	50					55					60					

tta	ttg	att	gtg	gca	tgc	aac	aca	gcg	agc	gct	cta	gct	tta	gaa	gag	240
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
65					70				75					80		

atg	caa	aag	cat	tcc	aaa	atc	cct	att	gtg	ggt	gtg	att	gag	cca	agc	288
Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser	
				85					90					95		

att	tta	gcg	atc	aaa	caa	caa	gta	aaa	gat	aaa	aac	gcc	cct	att	tta	336
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu	
			100					105					110			

gtg	tta	ggg	aca	aaa	gcg	acg	att	caa	tcc	aac	gct	tat	gac	aac	gcc	384
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala	
		115					120					125				

ctg	aaa	caa	caa	ggc	tat	ttg	aac	gtt	tcg	cat	tta	gcc	act	tct	ctt	432
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu	
	130					135					140					

ttt	gtg	cct	ttg	att	gaa	gaa	aat	att	tta	gag	ggc	gaa	ttg	tta	gaa	480
Phe	Val	Pro	Leu	Ile	Glu	Glu	Asn	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu	
145					150					155					160	

act	tgc	atg	cgt	tat	tat	ttc	act	cca	tta	gag	att	tta	cct	gaa	gtg	528
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val	
				165					170					175		

gtt	att	tta	ggt	tgc	acg	cat	ttt	ccc	ttg	atc	gct	cac	caa	att	gag	576
Val	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	His	Gln	Ile	Glu	
			180					185					190			

ggc	tat	ttt	atg	gag	cat	ttt	gcc	ctt	tca	acg	ccc	ccc	tta	ctc	atc	624
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Ser	Thr	Pro	Pro	Leu	Leu	Ile	
		195					200					205				

cat	tct	ggc	gat	gct	att	gtg	gaa	tat	ttg	caa	caa	aaa	tac	acc	ctt	672
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Thr	Leu	
	210					215					220					

aag	aaa	aat	gca	tgc	gcg	ttc	cct	aaa	gtg	gaa	ttt	cat	gcg	agc	ggc	720
Lys	Lys	Asn	Ala	Cys	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly	
											35					

225		230		235		240	
gat	gtg	gtt	tgg	cta	gaa	aaa	cag
Asp	Val	Val	Trp	Leu	Glu	Lys	Gln
				245			Ala
						Lys	250
						Glu	
						Trp	
						Leu	
						Lys	
						Leu	255
						taa	
							768

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 <212> PRT
 <213> H. pylori
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							Gly
							Gly
							Phe
							Ser
							15
							Val
							Leu
Lys	Ser	Leu	Leu	Lys	Ala	Gln	Ile
		20					25
							Phe
							Asp
							Glu
							Ile
							Ile
							Tyr
							30
							Tyr
							Gly
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly
		35					40
							Thr
							Lys
							Asp
							Pro
							45
							Thr
							Thr
							Ile
							Lys
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp
	50					55	
							Phe
							Phe
							Lys
							Pro
							60
							His
							Gln
							Ile
							Gly
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr
65					70		
							Ala
							Ser
							75
							Ala
							Leu
							Ala
							Leu
							Glu
							80
Met	Gln	Lys	His	Ser	Lys	Ile	Pro
				85			
							Ile
							Val
							90
							Gly
							Val
							Ile
							Glu
							95
							Pro
							Ser
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val
			100				
							Lys
							105
							Asp
							Lys
							Asn
							Ala
							110
							Pro
							Ile
							Leu
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile
		115					120
							Gln
							Ser
							Asn
							Ala
							125
							Tyr
							Asp
							Asn
							Ala
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn
	130					135	
							Val
							Ser
							His
							140
							Ala
							Thr
							Ser
							Leu
Phe	Val	Pro	Leu	Ile	Glu	Glu	Asn
145					150		
							Ile
							Leu
							Glu
							155
							Gly
							Glu
							Leu
							Leu
							Glu
							160
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr
				165			
							Pro
							Leu
							170
							Glu
							Ile
							Leu
							Pro
							175
							Glu
							Val
Val	Ile	Leu	Gly	Cys	Thr	His	Phe
			180				
							Pro
							185
							Leu
							Ile
							Ala
							His
							Gln
							190
							Ile
							Glu
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala
							200
							Leu
							Ser
							Thr
							Pro
							205
							Pro
							Leu
							Leu
							Ile

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Thr Leu
 210 215 220

Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240

Asp Val Val Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
 245 250 255

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 <211> 765
 <212> DNA
 <213> H. pylori

<221> CDS
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aaa agc ctt tta aaa gcg caa cta ttt gat gaa atc atc tat tat ggc 96
 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30

gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45

caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa 192
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
 50 55 60

tta ttg att gtg gca tgc aac acc gca agc gct ctg gct tta gaa gag 240
 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 65 70 75 80

atg caa aag cat tcc aaa atc cct gtt gtg ggc gtg att gag cca agc 288
 Met Gln Lys His Ser Lys Ile Pro Val Val Gly Val Ile Glu Pro Ser
 85 90 95

att tta gcg atc aaa cgg caa gtg aaa gat aaa aac gcc cct att ttg 336
 Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
 100 105 110

gtg cta ggg aca aaa gcg acg att caa tcc aac gcc tat gat aac gcc 384
 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
 115 120 125

ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt 432
 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
 130 135 140

ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg cta gaa 480
 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160

act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg 528
 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
 165 170 175

gtt att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag 576
Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
180 185 190

ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc 624
Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
195 200 205

cat tct ggc gat gct att gtg gaa tat ttg caa caa aat tac gcc ctt 672
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Asn Tyr Ala Leu
210 215 220

aag aaa aac gca tgc gcg ttc cct aaa gtg gaa ttt cat gcg agc ggc 720
Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
225 230 235 240

gat gtg gtt tgg cta gaa aaa caa gct aaa gaa tgg ctt aaa ttg 765
Asp Val Val Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
245 250 255

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<213> H. pylori

<400> 34

Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
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Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Val Val Gly Val Ile Glu Pro Ser
85 90 95

Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
165 170 175

Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Asn Tyr Ala Leu
210 215 220

Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
225 230 235 240

Asp Val Val Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
245 250 255

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<210> 36
<211> 28
<212> DNA
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<220>
<223> primer

<400> 36
agaattctat tacaatttga gccattct 28

<210> 37
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<400> 37
gcgaattcga tcagaatttt ttttct 26

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ataagtactt gtgaatctta tactag 26

<210> 39
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<212> DNA
<213> E. coli

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cgtcccaccg tgctggtggt tgactccggc gtcggtgggt tgctcggctta tgacgagatc 120
cggcatctct taccggatct ccattacatt tatgctttcg ataacgtcgc tttcccgtat 180
ggcgaaaaaa gcgaagcggt tattgttgag cgagtgggtg caattgtcac cgcggtgcaa 240
gaacgttatc cctttgcgct ggctgtgggt gcttgcaaca ctgccagtac cgtttcactt 300
cctgcattac gcgaaaagtt cgacttcccg gttgttggtg tcgtgccggc gattaaacct 360
gctgcacgtc tgacggcaaa tggcattgtc ggattactgg caaccgcgg aacagttaaa 420
cgttcttata ctcatgagct gatcgcgctt ttcgctaata atgccagat agaaatgctg 480
ggctcggcag agatggttga gttggctgaa gcgaagctac atggcgaaga tgtttctctg 540
gatgcactaa aacgtatcct acgcccgtgg ttaagaatga aagagccgcc agataccggt 600
gtattggggt gcacccatct cctctacta caagaagaac tgttacaagt gctgccagag 660
ggaacccggc tgggtggattc tggcgcagcg attgctcgcc gaacggcctg gttgttagaa 720
catgaagccc cggatgcaaa atctgccgat gcgaatattg ctttttgtat ggcaatgacg 780
ccaggagctg aacaattatt gcccgtttta cagcgttacg gcttcgaaac gctcgaaaaa 840
ctggcagttt taggctga 858

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<212> PRT
<213> E. coli

<400> 40

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Pro Ser Glu Pro Arg Pro Thr Val Leu Val Phe Asp Ser Gly Val Gly
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Gly Leu Ser Val Tyr Asp Glu Ile Arg His Leu Leu Pro Asp Leu His
35 40 45

Tyr Ile Tyr Ala Phe Asp Asn Val Ala Phe Pro Tyr Gly Glu Lys Ser
50 55 60

Glu Ala Phe Ile Val Glu Arg Val Val Ala Ile Val Thr Ala Val Gln
65 70 75 80

Glu Arg Tyr Pro Leu Ala Leu Ala Val Val Ala Cys Asn Thr Ala Ser
85 90 95

Thr Val Ser Leu Pro Ala Leu Arg Glu Lys Phe Asp Phe Pro Val Val
100 105 110

Gly Val Val Pro Ala Ile Lys Pro Ala Ala Arg Leu Thr Ala Asn Gly
115 120 125

Ile Val Gly Leu Leu Ala Thr Arg Gly Thr Val Lys Arg Ser Tyr Thr
130 135 140

His Glu Leu Ile Ala Arg Phe Ala Asn Glu Cys Gln Ile Glu Met Leu
145 150 155 160

Gly Ser Ala Glu Met Val Glu Leu Ala Glu Ala Lys Leu His Gly Glu
165 170 175

Asp Val Ser Leu Asp Ala Leu Lys Arg Ile Leu Arg Pro Trp Leu Arg
180 185 190

Met Lys Glu Pro Pro Asp Thr Val Val Leu Gly Cys Thr His Phe Pro
195 200 205

Leu Leu Gln Glu Glu Leu Leu Gln Val Leu Pro Glu Gly Thr Arg Leu
210 215 220

Val Asp Ser Gly Ala Ala Ile Ala Arg Arg Thr Ala Trp Leu Leu Glu
225 230 235 240

His Glu Ala Pro Asp Ala Lys Ser Ala Asp Ala Asn Ile Ala Phe Cys
245 250 255

Met Ala Met Thr Pro Gly Ala Glu Gln Leu Leu Pro Val Leu Gln Arg
260 265 270

Tyr Gly Phe Glu Thr Leu Glu Lys Leu Ala Val Leu Gly
275 280 285

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<212> DNA

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<210> 42
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<212> DNA
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<220>
<223> primer

<400> 42
agaattctat tacaatttga gccattct 28

<210> 43
<211> 822
<212> DNA
<213> E. faecalis

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aaggaagcgc taaagcaatt accaaatgaa cgattaatth attaggaga tacagcccgt 120
tgcccatatg gtccacgacc agccgaacaa gtcgttcagt ttacttggga aatggccgat 180
tttttattga aaaaacgaat aaaaatgcta gtaatcgcg gtaataccgc gacggctgtc 240
gcattagaag aaattaaagc tgccttgcca attccagttg ttggtgttat ttacctggc 300
gcacgagcag ccgttaaagt cacaaaaaat aacaaaattg gtgtcatagg taccttaggg 360
acaatcaaaa gtgtttccta tgaaatcgcc attaaaagta aggcaccagc aattgaggtg 420
actagtttag cttgccctaa atttgtcccc attgttgaaa gtaatcaata tcgttcttcc 480
gtagcaaaaa aaattgtggc agaaacactt caagcactac aattaaagg acttgatacg 540
ttgatttttag gttgtacca ttaccggtt ttacgtccgg tgattcaaaa tgtgatgggg 600
agtcattgtga cattaattga ctcaggagcc gaaacagttg gcgaagtcag catgcttctc 660
gattattttg acattgcca cagcctgaa gcgcctacac agcccatga atttataca 720
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aaagcacaac agattcactt aggaggaaac gaaaatgatt ag 822

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<211> 273
<212> PRT
<213> E. faecalis

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Leu Thr Val Leu Lys Glu Ala Leu Lys Gln Leu Pro Asn Glu Arg Leu
20 25 30

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Ile Tyr Leu Gly Asp Thr Ala Arg Cys Pro Tyr Gly Pro Arg Pro Ala
 35 40 45
 Glu Gln Val Val Gln Phe Thr Trp Glu Met Ala Asp Phe Leu Leu Lys
 50 55 60
 Lys Arg Ile Lys Met Leu Val Ile Ala Cys Asn Thr Ala Thr Ala Val
 65 70 75 80
 Ala Leu Glu Glu Ile Lys Ala Ala Leu Pro Ile Pro Val Val Gly Val
 85 90 95
 Ile Leu Pro Gly Ala Arg Ala Ala Val Lys Val Thr Lys Asn Asn Lys
 100 105 110
 Ile Gly Val Ile Gly Thr Leu Gly Thr Ile Lys Ser Ala Ser Tyr Glu
 115 120 125
 Ile Ala Ile Lys Ser Lys Ala Pro Ala Ile Glu Val Thr Ser Leu Ala
 130 135 140
 Cys Pro Lys Phe Val Pro Ile Val Glu Ser Asn Gln Tyr Arg Ser Ser
 145 150 155 160
 Val Ala Lys Lys Ile Val Ala Glu Thr Leu Gln Ala Leu Gln Leu Lys
 165 170 175
 Gly Leu Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro Leu Leu Arg
 180 185 190
 Pro Val Ile Gln Asn Val Met Gly Ser His Val Thr Leu Ile Asp Ser
 195 200 205
 Gly Ala Glu Thr Val Gly Glu Val Ser Met Leu Leu Asp Tyr Phe Asp
 210 215 220
 Ile Ala His Thr Pro Glu Ala Pro Thr Gln Pro His Glu Phe Tyr Thr
 225 230 235 240
 Thr Gly Ser Ala Lys Met Phe Glu Glu Ile Ala Ser Ser Trp Leu Gly
 245 250 255
 Ile Glu Asn Leu Lys Ala Gln Gln Ile His Leu Gly Gly Asn Glu Asn
 260 265 270

Asp

<210> 45

<211> 801
 <212> DNA
 <213> S. aureus

<400> 45
 atgaataaac caataggtgt aatagactct ggtgtcggag gtttgacagt agctaaagaa 60
 attatgcgtc agttgccaaa tgagacgatt tattacttag gtgatattgg gcgatgtcca 120
 tatggggccaa gaccaggaga acaagtaaaa caatatacag ttgaaatcgc tcgtaaatta 180
 atggaatttg atataaaaat gctcgtgatt gcttgtaata ctgcaactgc tgtagcttta 240
 gaatattttac aaaagacctt atcaatctca gtgattggcg taattgaacc aggtgctaga 300
 acagcaataa tgacgactag aaatcaaaat gtattagtac taggaacgga aggcacaatt 360
 aaatctgaag catatcgaac acatattaaa cgtataaatc cacatgtaga ggtacatggc 420
 gttgcctgtc cagggttttgt gccacttgta gaacaaatga gatatagtga tccaacaatt 480
 acaagcattg ttattcatca aacactgaaa cgttggcgta atagtgagtc tgatactgtc 540
 attttaggat gtaccacta tccattgctc tataaaccta tctatgatta ttttggtggt 600
 aaaaagacag tgatttcgtc tggattagaa acggctcgtg aagttagtgc attgctaaca 660
 tttagtaatg aacatgcaag ttatactgaa catccagatc atcgattttt tgcaacaggt 720
 gataccacac atattactaa cattatcaaa gaatggctaa atttatctgt caatgtggaa 780
 cgtatatcag tgaatgacta g 801

<210> 46
 <211> 266
 <212> PRT
 <213> S. aureus

<400> 46
 Met Asn Lys Pro Ile Gly Val Ile Asp Ser Gly Val Gly Gly Leu Thr
 1 5 10 15
 Val Ala Lys Glu Ile Met Arg Gln Leu Pro Asn Glu Thr Ile Tyr Tyr
 20 25 30
 Leu Gly Asp Ile Gly Arg Cys Pro Tyr Gly Pro Arg Pro Gly Glu Gln
 35 40 45
 Val Lys Gln Tyr Thr Val Glu Ile Ala Arg Lys Leu Met Glu Phe Asp
 50 55 60
 Ile Lys Met Leu Val Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu
 65 70 75 80
 Glu Tyr Leu Gln Lys Thr Leu Ser Ile Ser Val Ile Gly Val Ile Glu
 85 90 95

Pro Gly Ala Arg Thr Ala Ile Met Thr Thr Arg Asn Gln Asn Val Leu
 100 105 110
 Val Leu Gly Thr Glu Gly Thr Ile Lys Ser Glu Ala Tyr Arg Thr His
 115 120 125
 Ile Lys Arg Ile Asn Pro His Val Glu Val His Gly Val Ala Cys Pro
 130 135 140
 Gly Phe Val Pro Leu Val Glu Gln Met Arg Tyr Ser Asp Pro Thr Ile
 145 150 155 160
 Thr Ser Ile Val Ile His Gln Thr Leu Lys Arg Trp Arg Asn Ser Glu
 165 170 175
 Ser Asp Thr Val Ile Leu Gly Cys Thr His Tyr Pro Leu Leu Tyr Lys
 180 185 190
 Pro Ile Tyr Asp Tyr Phe Gly Gly Lys Lys Thr Val Ile Ser Ser Gly
 195 200 205
 Leu Glu Thr Ala Arg Glu Val Ser Ala Leu Leu Thr Phe Ser Asn Glu
 210 215 220
 His Ala Ser Tyr Thr Glu His Pro Asp His Arg Phe Phe Ala Thr Gly
 225 230 235 240
 Asp Thr Thr His Ile Thr Asn Ile Ile Lys Glu Trp Leu Asn Leu Ser
 245 250 255
 Val Asn Val Glu Arg Ile Ser Val Asn Asp
 260 265

<210> 47
 <211> 822
 <212> DNA
 <213> E. faecium

<400> 47
 atgatacgat tgacagataa tcgccctatc ggattttattg attcaggtgt cggcggccttg 60
 actgtagtaa aagaagccct gaaacaatta ccgaatgaaa atattttatt tgtaggagac 120
 acagcacgct gcccatatgg ccctagaccc gcggaacagg taatccagta tacttgggaa 180
 atgacggatt atctggtgga gcaaggaatc aagatgctgg tgatcgctg caataccgca 240
 actgcggtgg ctttagaaga aatcaaagct gctctttcta ttccagtcac cgggtgtgatc 300
 cttcccggta ctagagcggc agtaaaaaaa acacaaaata aacaagttgg cattatcggt 360
 acgattggta cggtaaaaag tcaagcttat gaaaaagcac tgaaagagaa agtaccagaa 420
 ttgactgtga caagtcttgc ttgtccaaaa ttgttttcag ttgtcgaaag taatgaatac 480

cattcatcgg tggcgaaaaa aattgtggca gaaacattag ctcttttaac cactaaaaaa 540
atcgatacat tgattttggg atgcacccat tatccattat tacgccccat cattcaaaat 600
gtaatgggag aaaatgttca actgatcgat tctggagcag aaacagtagg tgaagtatct 660
atgctgttag attattttcaa tctgagcaat tcaccgcaaa atgggtcggac attatgccag 720
ttttatacaa ctggctctgc caaacttttc gaggaatatag ctgaagactg gcttggaatc 780
ggacacttaa atgtagaaca tatcgaattg ggaggaaaat aa 822

<210> 48
<211> 273
<212> PRT
<213> E. faecium

<400> 48

Met Ile Arg Leu Thr Asp Asn Arg Pro Ile Gly Phe Ile Asp Ser Gly
1 5 10 15

Val Gly Gly Leu Thr Val Val Lys Glu Ala Leu Lys Gln Leu Pro Asn
20 25 30

Glu Asn Ile Leu Phe Val Gly Asp Thr Ala Arg Cys Pro Tyr Gly Pro
35 40 45

Arg Pro Ala Glu Gln Val Ile Gln Tyr Thr Trp Glu Met Thr Asp Tyr
50 55 60

Leu Val Glu Gln Gly Ile Lys Met Leu Val Ile Ala Cys Asn Thr Ala
65 70 75 80

Thr Ala Val Ala Leu Glu Glu Ile Lys Ala Ala Leu Ser Ile Pro Val
85 90 95

Ile Gly Val Ile Leu Pro Gly Thr Arg Ala Ala Val Lys Lys Thr Gln
100 105 110

Asn Lys Gln Val Gly Ile Ile Gly Thr Ile Gly Thr Val Lys Ser Gln
115 120 125

Ala Tyr Glu Lys Ala Leu Lys Glu Lys Val Pro Glu Leu Thr Val Thr
130 135 140

Ser Leu Ala Cys Pro Lys Phe Val Ser Val Val Glu Ser Asn Glu Tyr
145 150 155 160

His Ser Ser Val Ala Lys Lys Ile Val Ala Glu Thr Leu Ala Pro Leu
165 170 175

Thr Thr Lys Lys Ile Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro
 180 185 190
 Leu Leu Arg Pro Ile Ile Gln Asn Val Met Gly Glu Asn Val Gln Leu
 195 200 205
 Ile Asp Ser Gly Ala Glu Thr Val Gly Glu Val Ser Met Leu Leu Asp
 210 215 220
 Tyr Phe Asn Leu Ser Asn Ser Pro Gln Asn Gly Arg Thr Leu Cys Gln
 225 230 235 240
 Phe Tyr Thr Thr Gly Ser Ala Lys Leu Phe Glu Glu Ile Ala Glu Asp
 245 250 255
 Trp Leu Gly Ile Gly His Leu Asn Val Glu His Ile Glu Leu Gly Gly
 260 265 270

Lys

<210> 49
 <211> 335
 <212> DNA
 <213> E. saccharolyticus

<400> 49
 gcatgtaata cgcgaacggc ggtagcggtta gaagaaatta aagcgcaatt agatattcca 60
 gtcgtcgggtg tgatcttacc tgggtactcgt gctgcagtta aagctacgaa aaatcgtcaa 120
 atcgggtatta taggaacagc ggggtacaatt aaaagtagtt cgtatgagca agcaattaaa 180
 atgaaagtgc ctgaagcatc ggtgactagt ttagcttggtc cttaaatttgt accgattggt 240
 gaaagtaatc aatttcaatc atcggtagct aaaaaaattg ttgctgagac gttattacca 300
 ttgcaacata aaaaattaga tacgttgatt ttagg 335

<210> 50
 <211> 111
 <212> PRT
 <213> E. saccharolyticus

<400> 50

Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Ala Gln
 1 5 10 15

Leu Asp Ile Pro Val Val Gly Val Ile Leu Pro Gly Thr Arg Ala Ala
 20 25 30

Val Lys Ala Thr Lys Asn Arg Gln Ile Gly Ile Ile Gly Thr Ala Gly
 35 40 45

Thr Ile Lys Ser Ser Ser Tyr Glu Gln Ala Ile Lys Met Lys Val Pro
 Page 47

50

55

60

Glu Ala Ser Val Thr Ser Leu Ala Cys Pro Lys Phe Val Pro Ile Val
65 70 75 80

Glu Ser Asn Gln Phe Gln Ser Ser Val Ala Lys Lys Ile Val Ala Glu
85 90 95

Thr Leu Leu Pro Leu Gln His Lys Lys Leu Asp Thr Leu Ile Leu
100 105 110

<210> 51
<211> 344
<212> DNA
<213> E. mundtii

<400> 51
gtaatcgcat gtaataccgc aactgcggtc gcattagaag aaatcaaagc aacactctcg 60
attccagtga tcggtgtgat ttgcccagga acgagagcgg cagtcaagca gacgaaaaat 120
catcgagtag ggggtgattgg aacaattggt accgtcaaaa gtgctgctta cgagacggca 180
ttattggata aagcaccgga actgaaagtt accagcttgg cgtgtccaaa gtttgtttca 240
gtcgtagaaa gtaaagaata ccgatcatca gtcgctaaaa aaatcgtggc tcaaactttg 300
cttcattag aattaaaagg gatcgatacg ttgatttttag gttg 344

<210> 52
<211> 113
<212> PRT
<213> E. mundtii

<400> 52

Val Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys
1 5 10 15

Ala Thr Leu Ser Ile Pro Val Ile Gly Val Ile Leu Pro Gly Thr Arg
20 25 30

Ala Ala Val Lys Gln Thr Lys Asn His Arg Val Gly Val Ile Gly Thr
35 40 45

Ile Gly Thr Val Lys Ser Ala Ala Tyr Glu Thr Ala Leu Leu Asp Lys
50 55 60

Ala Pro Glu Leu Lys Val Thr Ser Leu Ala Cys Pro Lys Phe Val Ser
65 70 75 80

Val Val Glu Ser Lys Glu Tyr Arg Ser Ser Val Ala Lys Lys Ile Val
85 90 95

Ala Gln Thr Leu Leu Pro Leu Glu Leu Lys Gly Ile Asp Thr Leu Ile
Page 48

100

105

110

Leu

<210> 53
 <211> 340
 <212> DNA
 <213> E. casseliflavus

<400> 53
 atcgcacgta ataccgacgac agcgggtcgcc cttgaagaaa tcaaagaaca actaacgac 60
 ccagtgcacg gcgtgacccg gctggcagc cgagcagcag tcaaagcaag caaaaaccaa 120
 cgaatcggtg tcatcgggac aaacggaacg atcaaaagtg actcttataa gcgcgcgctt 180
 catggcaaag cgcacccatgc gtccgtcgtc agtttggtt gcccgagtt tgtgccgac 240
 gtagaaagca aacaatacca tagctcggtc gccaaagaaa tcgtggcaga aacgttgcgt 300
 ccattgaaaa acaaacggct agatacgttg attttaggtg 340

<210> 54
 <211> 112
 <212> PRT
 <213> E. casseliflavus

<400> 54

Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Glu
 1 5 10 15

Gln Leu Thr Ile Pro Val Ile Gly Val Ile Leu Pro Gly Ser Arg Ala
 20 25 30

Ala Val Lys Ala Ser Lys Asn Gln Arg Ile Gly Val Ile Gly Thr Asn
 35 40 45

Gly Thr Ile Lys Ser Asp Ser Tyr Lys Arg Ala Leu His Gly Lys Ala
 50 55 60

Pro His Ala Ser Val Val Ser Leu Ala Cys Pro Lys Phe Val Pro Ile
 65 70 75 80

Val Glu Ser Lys Gln Tyr His Ser Ser Val Ala Lys Lys Ile Val Ala
 85 90 95

Glu Thr Leu Arg Pro Leu Lys Asn Lys Arg Leu Asp Thr Leu Ile Leu
 100 105 110

<210> 55
 <211> 337
 <212> DNA
 <213> E. flavescens

<400> 55
 atcgcacgta ataccgacgac agcgggtcgcc cttgaagaaa tcaaagaaca actaacgac 60

ccagtgatcg gcgtgatcct gcctggcagt cgagcagcag tcaaagcaag caaaaaccaa 120
cgaatcggtg tcatcgggac aaacggaacg atcaaaagtg actcttataa gcgcgcgctt 180
catggcaaag cgcgccatgc gtccgtcgtc agtttggtt gcccgagtt tgtgccgatc 240
gtagaaagca aacaatacca tagctcggtc gccaaagaaa tcgtggcaga aacgttgcgt 300
ccattgaaaa acaaacggct agatacgttg atttttag 337

<210> 56
<211> 112
<212> PRT
<213> E. flavescens

<400> 56

Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Glu
1 5 10 15

Gln Leu Thr Ile Pro Val Ile Gly Val Ile Leu Pro Gly Ser Arg Ala
20 25 30

Ala Val Lys Ala Ser Lys Asn Gln Arg Ile Gly Val Ile Gly Thr Asn
35 40 45

Gly Thr Ile Lys Ser Asp Ser Tyr Lys Arg Ala Leu His Gly Lys Ala
50 55 60

Pro His Ala Ser Val Val Ser Leu Ala Cys Pro Lys Phe Val Pro Ile
65 70 75 80

Val Glu Ser Lys Gln Tyr His Ser Ser Val Ala Lys Lys Ile Val Ala
85 90 95

Glu Thr Leu Arg Pro Leu Lys Asn Lys Arg Leu Asp Thr Leu Ile Leu
100 105 110

<210> 57
<211> 341
<212> DNA
<213> E. cecorum

<400> 57

atcgcatgta ataccgcgac tgcagcagct ttaacccaaa ttaaggaaca attagacatt 60
ccagttgtcg gtgtgatttt acctggaact agagctgctg tcaaaaatac aaaatcgcaa 120
cgaattggga ttatcggcac acaaggaacc atccaaagtg gcagttatga acaagccatt 180
ctttctaaag taccgactgc tcaacctgtg agtttagcgt gtcctagatt tgttccgata 240
gtagaaagta atcaagcaaa ttcaagtgtg gcaaaaaaaaa ttgtcgtca aacactataa 300
ccgatgacga aaaaaaacat cgatacgttg atttttaggtt g 341

<210> 58

<211> 112
 <212> PRT
 <213> E. cecorum

<400> 58

Ile Ala Cys Asn Thr Ala Thr Ala Ala Ala Leu Thr Gln Ile Lys Glu
 1 5 10 15

Gln Leu Asp Ile Pro Val Val Gly Val Ile Leu Pro Gly Thr Arg Ala
 20 25 30

Ala Val Lys Asn Thr Lys Ser Gln Arg Ile Gly Ile Ile Gly Thr Gln
 35 40 45

Gly Thr Ile Gln Ser Gly Ser Tyr Glu Gln Ala Ile Leu Ser Lys Val
 50 55 60

Pro Thr Ala Gln Pro Val Ser Leu Ala Cys Pro Arg Phe Val Pro Ile
 65 70 75 80

Val Glu Ser Asn Gln Ala Asn Ser Ser Val Ala Lys Lys Ile Val Ala
 85 90 95

Gln Thr Leu Gln Pro Met Thr Lys Lys Asn Ile Asp Thr Leu Ile Leu
 100 105 110

<210> 59
 <211> 339
 <212> DNA
 <213> E. raffinosus

<400> 59

atcgcatgta ataccgcgac ggcagtagct ttggaagaaa ttaaaagaac cgtagatatt	60
cccgtaatcg gtgttatata gccaggatct cgcgcagcgt taaaggcaag cgaaaatggg	120
cgcgtgggaa ttatcggaac cattggaaca gtaaaaagtg gttcttataa acacgaacta	180
caggaaaaag ctctgatac ttatgtttct agtttagcat gcccaaaatt tgtaccgatt	240
gttgaaagta atcaatttaa tagctcggtg gcgaaaaaaa ttgtttctca aacattaact	300
cctttgaaaa aggaaaagtt ggatacgttg attttaggt	339

<210> 60
 <211> 112
 <212> PRT
 <213> E. raffinosus

<400> 60

Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Arg
 1 5 10 15

Thr Val Asp Ile Pro Val Ile Gly Val Ile Gln Pro Gly Ser Arg Ala
 20 25 30

Ala Leu Lys Ala Ser Glu Asn Gly Arg Val Gly Ile Ile Gly Thr Ile
 35 40 45

Gly Thr Val Lys Ser Gly Ser Tyr Lys His Glu Leu Gln Glu Lys Ala
 50 55 60

Pro Asp Thr Tyr Val Ser Ser Leu Ala Cys Pro Lys Phe Val Pro Ile
 65 70 75 80

Val Glu Ser Asn Gln Phe Asn Ser Ser Val Ala Lys Lys Ile Val Ser
 85 90 95

Gln Thr Leu Thr Pro Leu Lys Lys Glu Lys Leu Asp Thr Leu Ile Leu
 100 105 110

<210> 61
 <211> 341
 <212> DNA
 <213> E. malodoratus

<400> 61
 atcgcatgta ataccgcaac cgcagtggct ttagaagaga ttaagaagaa cgttgatatt 60
 cctggttattg gtgttatcca accaggatca cgtgctgcat taaaagcaag taaaaatagt 120
 cgtgtaggta tcatcggaac actaggaact gttaaaagtg gatcttataa acatgagctg 180
 caagaaaaag caccagaaac gtatgttgct agtctggcct gcccaaaatt tgtgccaatc 240
 gttgaaagta atcagtttaa tagttctgta gccaaaaaga ttgtttcaca atctctggca 300
 cccttaaaaa aggaaaaatt agatacgttg attttagggtt g 341

<210> 62
 <211> 112
 <212> PRT
 <213> E. malodoratus

<400> 62

Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Lys
 1 5 10 15

Asn Val Asp Ile Pro Val Ile Gly Val Ile Gln Pro Gly Ser Arg Ala
 20 25 30

Ala Leu Lys Ala Ser Lys Asn Ser Arg Val Gly Ile Ile Gly Thr Leu
 35 40 45

Gly Thr Val Lys Ser Gly Ser Tyr Lys His Glu Leu Gln Glu Lys Ala
 50 55 60

Pro Glu Thr Tyr Val Ala Ser Leu Ala Cys Pro Lys Phe Val Pro Ile
 65 70 75 80

Val Glu Ser Asn Gln Phe Asn Ser Ser Val Ala Lys Lys Ile Val Ser
85 90 95

Gln Ser Leu Ala Pro Leu Lys Lys Glu Lys Leu Asp Thr Leu Ile Leu
100 105 110

<210> 63
<211> 338
<212> DNA
<213> E. solitarus

<400> 63
gcatgtaata ccgcaacagc tgtggcttta gatgagatta aagagcaact gcaaatccct 60
gttgtgggag ttattatgcc ggaaccaga gcagctgta aagcgactaa aaatcatcgt 120
attggtgtga ttggcacaaa aggaacagtt aaaagtgctt cttacaaacg agcaatcaaa 180
gaaaaaatg aaaatacaaa agtaacaagt ttggcttgct cgaagtttgt tcccattgtg 240
gaaagtaatc aaattcattc ttcagtggca aaaaaattg tatttgaaac actattacc 300
ttaaaaaata aacatttaga tacgttgatt ttaggttg 338

<210> 64
<211> 111
<212> PRT
<213> E. solitarus

<400> 64

Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Asp Glu Ile Lys Glu Gln
1 5 10 15

Leu Gln Ile Pro Val Val Gly Val Ile Met Pro Gly Thr Arg Ala Ala
20 25 30

Val Lys Ala Thr Lys Asn His Arg Ile Gly Val Ile Gly Thr Lys Gly
35 40 45

Thr Val Lys Ser Ala Ser Tyr Lys Arg Ala Ile Lys Glu Lys Asn Glu
50 55 60

Asn Thr Lys Val Thr Ser Leu Ala Cys Pro Lys Phe Val Pro Ile Val
65 70 75 80

Glu Ser Asn Gln Ile His Ser Ser Val Ala Lys Lys Ile Val Phe Glu
85 90 95

Thr Leu Leu Pro Leu Lys Asn Lys His Leu Asp Thr Leu Ile Leu
100 105 110

<210> 65
<211> 341
<212> DNA

<213> E. hirae

<400> 65

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atcgcatgta ataccgctac tgcggttgct ttagaagaaa tcaaggcggc acttcctatt      60
ccagtcattg gtgtgatctt acctgggaca agagcagctg ttaaacaac aagaaataaa      120
caagtaggga ttatcggaac cctcggaacg atcaaaagtc gtgcttatga aacagcgctg      180
aaaacgaagg tacctgaact tgccgtgact agtttggtt gtccaaaatt cgtttcggtg      240
gtggaaagta atgaatatca ttcgtcagtg gcaaaaaaaaa tcgttgccca gacactagcg      300
ccattgggta ctaagaaaat cgatacgttg attttaggtt g                          341
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<210> 66

<211> 111

<212> PRT

<213> E. hirae

<400> 66

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Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Ala Ala
1          5          10          15
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```
Leu Pro Ile Pro Val Ile Gly Val Ile Leu Pro Gly Thr Arg Ala Ala
20          25          30
```

```
Val Lys Gln Thr Arg Asn Lys Gln Val Gly Ile Ile Gly Thr Leu Gly
35          40          45
```

```
Thr Ile Lys Ser Arg Ala Tyr Glu Thr Ala Leu Lys Thr Lys Val Pro
50          55          60
```

```
Glu Leu Ala Val Thr Ser Leu Ala Cys Pro Lys Phe Val Ser Val Val
65          70          75          80
```

```
Glu Ser Asn Glu Tyr His Ser Ser Val Ala Lys Lys Ile Val Ala Gln
85          90          95
```

```
Thr Leu Ala Pro Leu Val Thr Lys Lys Ile Asp Thr Leu Ile Leu
100          105          110
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<210> 67

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 67

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aaatagtcat atgaaaatag gcgtttttg      29
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<210> 68

<211> 28

<212> DNA

<213> Artificial Sequence

<220>
 <223> primer

 <400> 68
 agaattctat tacaatttga gccattct 28

 <210> 69
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 69
 gcgaattcga tcagaatttt ttttct 26

 <210> 70
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 70
 ataagtactt gtgaatctta tactag 26

 <210> 71
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 71
 aaaatgctag taatcgcatg taataccgc 29

 <210> 72
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 72
 tgggtacaac ctaaaatcaa cgtatc 26

 <210> 73
 <211> 765
 <212> DNA
 <213> Aquifex pyrophilus NA sequence

 <400> 73
 atgaagatag gtatctttga cagtgggtgtg gggggactta ctgttctaaa ggctataaga 60
 aatagataca gaaagggttga tatagtatac ctcgggtgata ccgcaagggt tccctacggc 120
 ataagggtcta aagatacgat aatcagatac tcccttgagt gtgcgggctt tttaaaggat 180
 aagggtgttg atataatcgt cgttgcctgc aataaccgaa gtgcttacgc tcttgaacgt 240

ttaaagaaag agataaacgt tcccgttttc ggcgttattg aaccgggggt taaagaagcc	300
ttaaaaaagt caaggaataa aaaaatagga gttataggaa ctctgcaac cgtaaaaagc	360
ggagcctacc agagaaagct tgaagagggg ggagctgatg tttttgcaa ggcctgtccc	420
ctattcgttc cccttgcgga ggaagggtctc cttgaggggg agataacaag aaagggttga	480
gaacactacc ttaaggagtt taaaggtaag attgatactc tgattttagg atgtacccat	540
tacccccctt ttaaaaagga gataaagaag tttttgggag acgttgaagt cgttgactct	600
tccgaagccc tttccctttc cctccataac ttataaagg acgatgggtc ctcacccctt	660
gagttatttt ttacggacct ttccccaat ctccagtttt tgattaaatt aatactcggt	720
agggattacc cggtaaaact tgcggagggg gtttttacac attaa	765

<210> 74
 <211> 262
 <212> PRT
 <213> Aquifex pyrophilus amino acid sequence

<400> 74

Met	Lys	Ile	Gly	Ile	Phe	Asp	Ser	Gly	Val	Gly	Gly	Leu	Thr	Val	Leu
1				5					10					15	

Lys	Ala	Ile	Arg	Asn	Arg	Tyr	Arg	Lys	Val	Asp	Ile	Val	Tyr	Leu	Gly
			20					25					30		

Asp	Thr	Ala	Arg	Val	Pro	Tyr	Gly	Ile	Arg	Ser	Lys	Asp	Phe	Thr	Thr
		35					40					45			

Ile	Ile	Arg	Tyr	Ser	Leu	Glu	Cys	Ala	Gly	Phe	Leu	Lys	Asp	Lys	Gly
	50					55					60				

Val	Asp	Ile	Ile	Val	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Tyr	Ala	Leu
65					70					75					80

Glu	Arg	Leu	Lys	Lys	Glu	Ile	Asn	Val	Pro	Val	Phe	Gly	Val	Ile	Glu
			85						90					95	

Pro	Gly	Val	Lys	Glu	Ala	Leu	Lys	Lys	Ser	Phe	Thr	Arg	Asn	Lys	Lys
			100					105					110		

Ile	Gly	Val	Ile	Gly	Thr	Pro	Ala	Thr	Val	Lys	Ser	Gly	Ala	Tyr	Gln
		115					120					125			

Arg	Lys	Leu	Glu	Glu	Gly	Gly	Ala	Asp	Val	Phe	Ala	Lys	Ala	Cys	Pro
	130					135					140				

Leu	Phe	Val	Pro	Leu	Ala	Glu	Glu	Gly	Leu	Leu	Glu	Gly	Glu	Ile	Thr
145					150					155					160

Arg Lys Val Val Glu His Tyr Phe Thr Leu Lys Glu Phe Lys Gly Lys
165 170 175

Ile Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro Leu Leu Lys Lys
180 185 190

Glu Ile Lys Lys Phe Leu Gly Asp Val Glu Val Val Asp Ser Ser Glu
195 200 205

Ala Leu Ser Leu Ser Leu His Asn Phe Ile Lys Asp Asp Gly Ser Ser
210 215 220

Ser Leu Glu Leu Phe Thr Phe Phe Thr Asp Leu Ser Pro Asn Leu Gln
225 230 235 240

Phe Leu Ile Lys Leu Ile Leu Gly Arg Asp Tyr Pro Val Lys Leu Ala
245 250 255

Glu Gly Val Phe Thr His
260

<210> 75
<211> 19
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19

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<400> 76
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18

<210> 77
<211> 62
<212> PRT
<213> Staphylococcus aureus

<400> 77

Ile Leu Pro Gly Ala Arg Ala Ala Val Lys Val Thr Lys Asn Asn Lys
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Ile Gly val Ile Gly Thr Leu Gly Thr Ile Lys Ser Ala Ser Tyr Asp
20 25 30

Ile Ala Ile Lys Ser Lys Ala Pro Ala Ile Glu Val Thr Ser Leu Ala
35 40 45

Cys Pro Lys Phe Val Pro Ile Val Glu Ser Asn Gln Tyr Arg
50 55 60

<210> 78
<211> 62
<212> PRT
<213> Enterococcus faecalis

<400> 78

Ile Glu Pro Gly Ala Arg Thr Ala Ile Met Thr Thr Arg Asn Gln Asn
1 5 10 15

Val Leu Val Leu Gly Thr Glu Gly Thr Ile Lys Ser Glu Ala Tyr Arg
20 25 30

Thr His Ile Lys Arg Ile Asn Pro His Val Glu Val His Gly Val Ala
35 40 45

Cys Pro Gly Phe Val Pro Leu Val Glu Gln Met Arg Tyr Ser
50 55 60

<210> 79
<211> 49
<212> PRT
<213> Staphylococcus aureus

<400> 79

Ser Val Ala Lys Lys Ile Val Ala Glu Thr Leu Gln Ala Leu Gln Leu
1 5 10 15

Lys Gly Leu Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro Leu Leu
20 25 30

Arg Pro Val Ile Gln Asn Val Met Gly Ser His Val Thr Leu Ile Asp
35 40 45

Ser

<210> 80
<211> 49
<212> PRT
<213> Enterococcus faecalis

<400> 80

Thr val Ile Ser Ile val Ile His Gln Thr Leu Lys Arg Trp Arg Asn
1 5 10 15

Ser Glu Ser Asp Thr Val Ile Leu Gly Cys Thr His Tyr Pro Leu Leu
20 25 30

Tyr Lys Pro Ile Tyr Asp Tyr Phe Gly Gly Lys Lys Thr Val Ile Ser
35 40 45

Ser

<210> 81
<211> 62
<212> PRT
<213> Staphylococcus aureus

<400> 81

Ile Leu Pro Gly Thr Arg Ala Ala Val Lys Lys Thr Gln Asn Lys Gln
1 5 10 15

Val Gly Ile Ile Gly Thr Ile Gly Thr Val Lys Ser Gln Ala Tyr Glu
20 25 30

Lys Ala Leu Lys Glu Lys Val Pro Glu Leu Thr Val Thr Ser Leu Ala
35 40 45

Cys Pro Lys Phe Val Ser Val Val Glu Ser Asn Glu Tyr His
50 55 60

<210> 82
<211> 62
<212> PRT
<213> Enterococcus faecium

<400> 82

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1 5 10 15

Val Leu Val Leu Gly Thr Glu Gly Thr Ile Lys Ser Glu Ala Tyr Arg
20 25 30

Thr His Ile Lys Arg Ile Asn Pro His Val Glu Val His Gly Val Ala
35 40 45

Cys Pro Gly Phe Val Pro Leu Val Glu Gln Met Arg Tyr Ser
50 55 60

<210> 83
<211> 15
<212> PRT
<213> Staphylococcus aureus

<400> 83

Ser Val Ala Lys Lys Ile Val Ala Glu Thr Leu Ala Pro Leu Thr
Page 59

1 5 10 15

<210> 84
<211> 15
<212> PRT
<213> Enterococcus faecium

<400> 84

Thr val ile ser ile val ile his gln thr leu lys arg trp arg
1 5 10 15

<210> 85
<211> 32
<212> PRT
<213> Staphylococcus aureus

<400> 85

lys lys ile asp thr leu ile leu gly cys thr his tyr pro leu leu
1 5 10 15

arg pro ile ile gln asn val met gly glu asn val gln leu ile asp
20 25 30

<210> 86
<211> 32
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<400> 86

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20 25 30

<210> 87
<211> 111
<212> PRT
<213> Enterococcus faecalis

<400> 87

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1 5 10 15

val gly ile ile gly thr ile gly thr val lys ser gln ala tyr glu
20 25 30

lys ala leu lys glu lys val pro glu leu thr val thr ser leu ala
35 40 45

cys pro lys phe val ser val val glu ser asn glu tyr his ser ser
Page 60

50

55

60

Val Ala Lys Lys Ile Val Ala Glu Thr Leu Ala Pro Leu Thr Thr Lys
65 70 75 80

Lys Ile Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro Leu Leu Arg
85 90 95

Pro Ile Ile Gln Asn Val Met Gly Glu Asn Val Gln Leu Ile Asp
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<210> 88

<211> 111

<212> PRT

<213> Enterococcus faecium

<400> 88

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Ile Gly Val Ile Gly Thr Leu Gly Thr Ile Lys Ser Ala Ser Tyr Asp
20 25 30

Ile Ala Ile Lys Ser Lys Ala Pro Ala Ile Glu Val Thr Ser Leu Ala
35 40 45

Cys Pro Lys Phe Val Pro Ile Val Glu Ser Asn Gln Tyr Arg Ser Ser
50 55 60

Val Ala Lys Lys Ile Val Ala Glu Thr Leu Gln Ala Leu Gln Leu Lys
65 70 75 80

Gly Leu Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro Leu Leu Arg
85 90 95

Pro Val Ile Gln Asn Val Met Gly Ser His Val Thr Leu Ile Asp
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<210> 89

<211> 63

<212> PRT

<213> Staphylococcus aureus

<400> 89

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1 5 10 15

Val Leu Val Leu Gly Thr Glu Gly Thr Ile Lys Ser Glu Ala Tyr Arg
20 25 30

Thr His Ile Lys Arg Ile Asn Pro His Val Glu Val His Gly Val Ala
35 40 45

Cys Pro Gly Phe Val Pro Leu Val Glu Gln Met Arg Tyr Ser Asp
50 55 60

<210> 90
<211> 63
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<213> Enterococcus faecalis

<400> 90

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1 5 10 15

Ile Gly Val Ile Gly Thr Leu Gly Thr Ile Lys Ser Ala Ser Tyr Asp
20 25 30

Ile Ala Ile Lys Ser Lys Ala Pro Ala Ile Glu Val Thr Ser Leu Ala
35 40 45

Cys Pro Lys Phe Val Pro Ile Val Glu Ser Asn Gln Tyr Arg Ser
50 55 60

<210> 91
<211> 63
<212> PRT
<213> Enterococcus faecium

<400> 91

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Val Gly Ile Ile Gly Thr Ile Gly Thr Val Lys Ser Gln Ala Tyr Glu
20 25 30

Lys Ala Leu Lys Glu Lys Val Pro Glu Leu Thr Val Thr Ser Leu Ala
35 40 45

Cys Pro Lys Phe Val Ser Val Val Glu Ser Asn Glu Tyr His Ser
50 55 60

<210> 92
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<400> 92

Thr Val Ile Ser Ile Val Ile His Gln Thr Leu Lys Arg Trp Arg
1 5 10 15

<210> 93
<211> 15
<212> PRT
<213> Enterococcus faecalis

<400> 93

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1 5 10 15

<210> 94
<211> 15
<212> PRT
<213> Enterococcus faecium

<400> 94

Ser Val Ala Lys Lys Ile Val Ala Glu Thr Leu Ala Pro Leu Thr
1 5 10 15

<210> 95
<211> 32
<212> PRT
<213> Staphylococcus aureus

<400> 95

Ser Glu Ser Asp Thr Val Ile Leu Gly Cys Thr His Tyr Pro Leu Leu
1 5 10 15

Tyr Lys Pro Ile Tyr Asp Tyr Phe Gly Gly Lys Lys Thr Val Ile Ser
20 25 30

<210> 96
<211> 32
<212> PRT
<213> Enterococcus faecalis

<400> 96

Lys Gly Leu Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro Leu Leu
1 5 10 15

Arg Pro Val Ile Gln Asn Val Met Gly Ser His Val Thr Leu Ile Asp
20 25 30

<210> 97
<211> 32
<212> PRT
<213> Enterococcus faecium

<400> 97

Lys Lys Ile Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro Leu Leu
1 5 10 15

Arg Pro Ile Ile Gln Asn Val Met Gly Glu Asn Val Gln Leu Ile Asp
20 25 30